RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/765,061_   _# 7½_

Source: _OIPE_

Date Processed by STIC: _8/15/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

OIPE

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION   US/09/765,061

DATE: 08/15/2001
TIME: 11:44:00

INPUT SET: S36601.raw

Does Not Comply
Corrected Diskette Needed

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

use upper-case letters for headings

insert these mandatory headings and responses for a U.S. case

```
1         GENERAL INFORMATION:        SEQUENCE LISTING
2
3    (1)   General Information
-->  4          (iii) NUMBER OF SEQUENCES: 1
```

                                                    (i) APPLICANT:
                                                    (ii) TITLE OF INVENTION:

                                                    (iv) CORRESPONDENCE ADDRESS:
                                                         (A) ADDRESSEE:
                                                         (B) STREET:
                                                         (C) CITY:
                                                         (D) STATE:
                                                         (E) COUNTRY:
                                                         (F) ZIP:
                                                    (v) COMPUTER READABLE FORM:
                                                         (A) MEDIUM TYPE:
                                                         (B) COMPUTER:
                                                         (C) OPERATING SYSTEM:
                                                         (D) SOFTWARE:
                                                    (vi) CURRENT APPLICATION DATA:
                                                         (A) APPLICATION NUMBER:
                                                         (B) FILING DATE:

78
(p.13)

ERRORED SEQUENCES FOLLOW:

see pp 1-14

```
5         (2) INFORMATION FOR SEQ ID NO:1:
6              (i) SEQUENCE CHARACTERISTICS:
-->  7              (A)  LENGTH: 6749 bases
8                   (B)  TYPE: nucleic acid
9                   (C)  STRANDEDNESS: single
10                  (D)  TOPOLOGY: linear
```

6689 (p.3)

For bases

```
11             (ii) MOLECULE TYPE: DNA (genomic) human
12             (ix) FEATURE:
13                  (A ) NAME/KEY: AIPL1 gene
14                  (B) LOCATION: 17p13.1
15                  (D) OTHER INFORMATION: produces aryl-hydrocarbon
16                  receptor interacting protein-like 1
17             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
18
19   ggcctcccaa agtgctggat tacaggcgtg agtcaccgcg cctggtcccc tgtcttcttt   60
20   aagaaagctc agcggacctt tttccttctt ggggtggaac aaaaagccaa atctagcaca  120
21   accctgggca ggggcccaga atcactggaa gcaaaggtgg atgggatagg aggcgaggct  180
22   gcctgtggac cacaggcccg gcccgagtgg ctctgatgag aagccggggc gcctaggtca  240
23   ccgcccccac cgtctgccct tcccccccact cctcctggct gggtaaatcc cagagtctca  300
24   gccgcctaag tgtcttcccc ggaggtgaga ttatctccgc ctgtgctgga cacctccctt  360
25   tctcctgcag ccatggatgc cgctctgctc ctgaacgtgg aaggggtcaa gaaaaccatt  420
26   ctgcacgggg gcacgggcga gctcccaaac ttcatcaccg gatcccgagt gagtggggcc  480
27   cctccggagc agacagggtc ccccacagca gctttcaaca ttccaggtgt gccccaaggc  540
28   actgtaaaca gctttcagct gtgccaaaaa aacagccagg cagccccagc gctgggcctc  600
29   cggggagctc ccagcgttta cccattcagg gggcattttt ggtactttgc agattcaact  660
30   ttagcatggg ctgaggggaa gggctttttgg gaattttctg gggccctaaa tgttgagtga  720
31   gaagaaaggg agtccgagga gtcttggtat ttgtccccaa atgtctgtta ggcttccctg  780
32   gactgaaggg tgcgtctgtg gctacagaat tcgggctttg gccaggcgag gcggctcccg  840
33   cctgtaatcc cagcactttg ggaggccaag atgggcagat catgaggtca agagttcgag  900
34   accagcctga ccaacatgtg aaaccccatc tctactgaaa atacaaaaat tagccagatg  960
35   tgctgtggcg cctgtaatcc cagttcagat actcaggaga cttgaggcag gagaatcact 1020
36   tgagcccagg aggtggaggt tgcagtgagc cgagatcata ccactgcact ccaacctggg 1080
37   caacagagtg agactctgtc tcagaaaaaa aaaaaaaaaa aagaactcgg gcttacttga 1140
38   ggaaggattt ctggacgcac agggctgtgg ggagtggaat ggggtctgta gggaggggtg 1200
39   ggtccctcct ccctgggggg tgcaggcagg gtggaggtgc tccaggggtc tgaggcatct 1260
```

use upper-case letters when using old sequence Ruler format

FYI! all U.S. cases filed on or after July 1, 1998, and which cannot claim a prior application filed before July 1, 1998, need to be in new Sequence Ruler format.

INPUT SET: S36601.raw

```
40   gatggggtga actgagtgag ctgaccctgg ggacagccct gggtgtcggt ggcaagggg  1320
41   tggcttctgc cgggccttga acagtgtgtc tagagcagag tgcaccgtct cggtgactag  1380
42   gtgatctttc atttccgcac catgaaatgt gatgaggagc ggacagtcat tgacgacagt  1440
43   cggcaggtgg gccagcccat gcacatcatc atcggaaaca tgttcaagct cgaggtctgg  1500
44   gagatcctgc ttacctccat gcgggtgcac gaggtggccg agttctggtg cgacaccatc  1560
45   gtaagtaggc cctgcgcgcc tgtctcctgg gactagtctt ttctgggctc acccacccgc  1620
46   tttgcggggc tgctgtgttt cgggaaagct gggactcaag cgaagctttg caaagccagt  1680
47   cctgcaaact tattccccac cgtgtgcatg tgaagatgga gggaacaagg gctggaaggg  1740
48   gtgacccatg ctgtggctgg ctggtgggga gcagggctat gaccagcagg agtgagctgg  1800
49   cccacttcac agtcctcaca tctgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg  1860
50   tgtgtgtgtg agagagagag agagagagag agagagnnnn nnnnnntagc cttaggactt  1920
51   attgcagaga ccaacaccta acaatgtaat caggcagcca gtgcaggaca taaataagta  1980
52   aggcagtgtg ctttgggcca caaaagcacg ctcagcttgc tggaagccat gggtgccgag  2040
53   ctgggggctg ctgagtcagg gccaaagggg gcccctccct gcagtaagct ggttctgggg  2100
54   cctctccctc ccttggtcca gctcttaatc ccaacaggct caacagccat ctgcttgtct  2160
55   cttccataaa gaggcagaag gcatttcggg ctaatcccgg ccggtggggc gggcagggtg  2220
56   acctctgtct ctgtgctggt gacctggagg cagagctgaa ctgctgcata gagtttcagc  2280
57   cccttcactt cacatgttgc atgtggggcc agtgctgggt catctcagaa gccggtccaa  2340
58   ggagatgggt tctcagggag cctagttggg gaaactgagg cccagcatac atacagcagg  2400
59   cctcgctgag gccgcacggc ggatcttccc agccctcctt catcccaagg gtggcaaact  2460
60   cagctcccat gctggctgaa gctgtgatga gccagatcta tatctgcacc atctcattta  2520
61   atccctacag cagccctaat atcgaacagg agcaacccag ggaactgagt ttcagagaag  2580
62   tgcagagacc tgggctcacc gctaacctgc agcactgcca ggacaccaaa gcgactctct  2640
63   tggaccctgg agtcctgctc cttctactgc cccacactgc ccttcctgcg agtcataggc  2700
64   tttgcagagg tcagggtttc cctggggcag agatgtgtta cagtggacca caagggccag  2760
65   aagaggcagc cggaggctaa cagcatatgg cctctggagc caggtttgaa tcctggctgc  2820
66   gtcatttcct agctgtgtga ccttaagcaa gttgcttgcg tctctgggct gtagtttccc  2880
67   catccgtaaa atgggataat agtgcctgcc ttgaattgtc ataaggattg aaggggctca  2940
68   taacagtgtg aagtgctttg cctggcacac agttaaccac agttagtatg agtggcatag  3000
69   tgagggagca ggattcctcc caggaggggc tctgagtgga ggccttttat ggcccaccta  3060
70   gctctgggca ggtagcctgg atgccatcca tccgtttatc cccacagcac acggggtct   3120
71   accccatcct rtcccggagc ctgaggcaga tggcccaggg caaggacccc acagagtggc  3180
72   acgtgcacac gtgcgggctg gccaacatgt tcgcctacca cacgctgggc tacgaggacc  3240
73   tggacgagct gcagaaggag cctcagcctc tggtctttgt gatcgagctg ctgcaggtgg  3300
74   ggctggggtt ggcagggctg gagggctgtg ccagcactgg agagggacag cgggcatcat  3360
75   gggcacccccc accccactgg ccactggaca gtgccctgtt tctgtttaga taatacgaga  3420
76   gggttcataa gccatgggag aatacgaatt tgaaaaaaaa gtcctctgat ttttccacaa  3480
77   gaaaagtcct ttggtgctgg gcatggtggc ccacgcctgt aatcctagca ctttgggagg  3540
78   ccgagggggt tggatcacct gaggtcagga gttcgaagac cagcctggcc aacatggtaa  3600
79   aaccccgtct ctattaaaaa cacaaaaatt aaccgggtgt ggtggtgcat gcctgtaatc  3660
80   aatcccagct acttgggaat ttgaggcatg agaattgctt gaacctggaa gtggaggttg  3720
81   cagtgagcag agatcatgtc agtgcatttt aacctgggtg acagagtgag actccatgtc  3780
82   caaaaaaaag aaaaaaaaaa aaagtccact tggaaccagt ttttaaaaat gtgattcatt  3840
83   ttcattgtgg aggcatttta tccacttcca cttttcatttt caggagttgg agattataac  3900
84   cgcctccttg gttcctgtgg tttgtgggtt cagacttggt tctctngtgg cgggagaggc  3960
85   tgcatggaac tccccacatc ctcccaacca ggagccccag agtgattggc agcgcgtgtt  4020
86   tgtggattgg tgagagaggg ttagggccag ggtcaaggtc aggtcaggac tcagcttatg  4080
87   gccaagactg aggctcagcc tgagagctat gtgggtgaat aaaataaaat aagaactgtg  4140
88   tcaaccaagg gccccttaca ggcttgctgt cacagttgtg tggtctgtgc actgcacaag  4200
89   gtgcaccggc atctcctcca aggtgctcat tatagacatt gtatattggt atttccataa  4260
90   tgagaagttt ccagcagatg gcaatagtgt attgttctaa caaaacgagt attcgtgaca  4320
91   attttctgaa tattagaagt gaagtgtctt gatgaacggg cacctttttcc tagtttgcac  4380
92   aaagacattg atttagggca gggttttcgg cgttgttgct tctttccctt gtctgtatgc  4440
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INPUT SET: S36601.raw

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       93  acttgaccag caagcatgac ttcagggaga tgtgccacag ggtcctgttt ttcgggtctc 4500
       94  tgatgggggtg caggcccctg gggtccctgc ctcactgacc tgcagctctg gggccaggtt 4560
       95  gatgccccga gtgattacca gagggagacc tggaacctga gcaatcatga gaagatgaag 4620
       96  gcggtgcccg tcctccacgg agagggaaat cggctcttca agctgggccg ctacgaggag 4680
       97  gcctcttcca agtaccagga ggccatcatc tgcctaagga acctgcagac caaggtcaga 4740
       98  ggccgctggc caggggtggg aagtggcgct gactctgggg ggcctgccca gtgccggcca 4800
       99  gggtgggggcg ggggttgggc agctgcctga ggtcatggct gaccttctcc ctgggcagga 4860
      100  gaagccatgg gaggtgcagt ggctgaagct ggagaagatg atcaatactc tgatcctcaa 4920
      101  ctactgccag tgcctgctga agaaggagga gtactatgag gtgctggagc acaccagtga 4980
      102  tattctccgg caccacccag gtgcgcgggg ctgcaggggc ggacagtgag ggggcgccca 5040
      103  gcccagggcc acggagacac ctgccatagc cttcctggac ttttctttcc accccaccag 5100
      104  ggcaccaaac cttgtctcca cccagccggg tttccccgag tgtgtaactg aattgtgggt 5160
      105  gatggatggg cagtgcttgg cgcggggcgg cctttatttt aatgtgtgtt tgaacactta 5220
      106  cccaggaagc tcgccaagct tgtgatttca gcggaacggt aaacaggcgt ttaaaaagag 5280
      107  gggcaatcaa tatagggaaa aatattatga tgtcggtact agtactggtg ttgcgaggat 5340
      108  atggcaccgc agtactagat tgacttaatg ctcgaatcgt gctcacagta aaaacatcca 5400
      109  gcccctggct catgcatcag gcacacgtcg tctgcgttta ttatctcatt taatcctcat 5460
      110  aatcctcata atcaccatat gagggaggtg cagggaaagg ggcctgaagg ttatctaatt 5520
      111  taggtagcgt ctataagaaa aataaaacaa agttatgaat ataaaattac tcacagggcc 5580
      112  ttaaaaagga gaggaggagg tactgctatt atgatcatca tctccatctt acagttgagg 5640
      113  aaaccgaggg atgggggata cagagaggtt aaggatcatg gcggggctga gggtcttgga 5700
      114  ggctggtgag tcccagctgg gctggggctg cctctgaggc tgggaaggga gctgtagctg 5760
      115  gatgctccct gctccccaca ggcatcgtga aggcctacta cgtgcgtgcc cgggctcacg 5820
      116  cagaggtgtg gaatgaggcc gaggccaagg cggacctcca gaaagtgctg gagctggagc 5880
      117  cgtccatgca gaaggcggtg cgcagggagc ttgaggctgc tggagaaccg catggcggag 5940
      118  aacaggagga ggagcggctg cgctgccgga acatgctgag ccagggtgcc acgcagcctc 6000
      119  ccgcagagcc acccacagag ccacccgcac agtcatccac agagccacct gcagagccac 6060
      120  ccacagcacc atctgcagag ctgtccgcag ggcccccctgc agagccagcc acagagccac 6120
      121  ccccgtcccc agggcactcg ctgcagcact gagcccccctg aggcccacag ccacccaggc 6180
      122  agggagcaag tggcctggtc acttctggtt cgattgacca ggatcgtggt gtcactttt t 6240
      123  aaaatttaaa attaatttt gaaatcaaag tcagacacac ccatggtaaa aaaaaaaaa 6300
      124  aaaacaatcc caagggtaca gaagagctta tgaataaaag tagttttctc ctctaccccct 6360
      125  ctcattcctt ccgtgccatg gtttaattg accctgtttt taattcttct ggtagttttc 6420
      126  tctatttcca agtaatctgt ttaaatcagt ttctagattt taccccatgt caatgacaaa 6480
      127  tgaggatttg atgctctgat cctttctcat gcctgatacc cctccctgtc tccccatttt 6540
      128  ggatagttac atttgggggt catctcggtg attttttgtaa ctttacgcag gacacttaga 6600
      129  gctctctaga atcccactga ctttagtggg gtcttgatgt agggtgggca agccccgaca 6660
-->   130  ctggagctta gcctgagagg ggttcttgc                                    6749
      131
```

───

```
      334          (2) INFORMATION FOR SEQ ID NO:8:
      335              (i) SEQUENCE CHARACTERISTICS:
-->   336                  (A) LENGTH: 1129 bases
      337                  (B) TYPE: nucleic acid
      338                  (C) STRANDEDNESS: single
      339                  (D) TOPOLOGY: linear
      340             (ii) MOLECULE TYPE: cDNA Squirrel monkey
      341             (ix) FEATURE:
      342                  (A ) NAME/KEY: AIPL1 gene
      343                  (B) LOCATION:
      344                  (D) OTHER INFORMATION: produces aryl-hydrocarbon
      345                      receptor interacting protein-like 1
      346             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
```

```
347
348    atggatgccg ctctgctcct gaacgtggaa ggggtcaaga agaccattct gcacgggggc    60
349    acgggcgagc tcccaaattt catcaccgga tcccgagtga tctttcattt ccgcaccatg   120
350    aaatgtgatg aggagcggac ggtgattgac gacagcaggg aggtgggcca gcccatgcac   180
351    atcatcatcg gaacatgtt caagctggag gtctgggaga tcctgctcac gtccatgcgg    240
352    gtgcgagagg tggccgagtt ctggtgcgac accatccaca cgggggtcta ccccatcctg   300
353    tcccggagcc tgcggcagat ggcccagggc aaggacccga cggagtggca tgtgcacacg   360
354    tgcgggctgg ccaacatgtt cgcctaccac acgctgggct acgaggacct ggatgagctg   420
355    cagaaggagc ctcagcctct gatctttgtg atcgagctgc tgcaggttga tgccccaagt   480
356    gattaccaga gggagacctg gaacctgagc aatcacgaga agatgaaggt ggtgcccgtc   540
357    ctccatggag aaggaaatag gctcttcaag ctgggccgct acgaggaggc ctcttccaag   600
358    taccaggagg ccatcatctg cctaaggaac ctgcagacca aggagaaacc ctgggaggtg   660
359    cagtggctga agctggagaa gatgatcaat accctgatcc tcaactactg tcagtgtctg   720
360    ctgaagaagg aggagtacta cgaggtcctg gagcatacca gtgacattct ccggcaccac   780
361    ccaggcattg tgaaggccta ctatgtgcgc gcccgggctc acgcggaggt gtggaacgag   840
362    gccgaggcca aggcggacct ccagaaagtg ctggagctgg agccgtccat gcagaaggcg   900
363    gtgcgcaggg agctgaggct gctggagaac cgcatggcgg agaagcagga ggaggagcgg   960
364    ctgcgctgcc gcaacatgct gagccagggg gccacgtggt cccccgcgga gccacccgca  1020
365    gagccacctg cagagtcatc cacagagcca cccgcagagc cacctgcaga gccacctgca  1080
366    gagctaacct tgaccccggg gcacccacta cagcactga                          1129
367
```

```
913        (2) INFORMATION FOR SEQ ID NO:42:
914            (i) SEQUENCE CHARACTERISTICS:
915                (A) LENGTH: 20 bases
916                (B) TYPE: nucleic acid
917                (C) STRANDEDNESS: single
918                (D) TOPOLOGY: linear
919            (ii) MOLECULE TYPE: DNA Primer
920            (ix) FEATURE:
921                (A ) NAME/KEY: AIPL1 primer
922                (B) LOCATION:
923                (D) OTHER INFORMATION: 5' to 3' order
924            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:
925
926                5'-gagaaaaccattctgcacgg-3'                                20
927
```

```
928        (2) INFORMATION FOR SEQ ID NO:43:
929            (i) SEQUENCE CHARACTERISTICS:
930                (A) LENGTH: 19 bases
931                (B) TYPE: nucleic acid
932                (C) STRANDEDNESS: single
933                (D) TOPOLOGY: linear
934            (ii) MOLECULE TYPE: DNA Primer
935            (ix) FEATURE:
936                (A ) NAME/KEY: AIPL1 primer
937                (B) LOCATION:
938                (D) OTHER INFORMATION:
939            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:
940
941                5'-tgcagctcgtccaggtcct-3'                                 19
942
```

PAGE: 5

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/09/765,061*

DATE: 08/15/2001
TIME: 11:44:02

INPUT SET: S36601.raw

```
943            (2) INFORMATION FOR SEQ ID NO:44:
944                (i) SEQUENCE CHARACTERISTICS:
-->   945            (A) LENGTH: 17 bases
946                    (B) TYPE: nucleic acid
947                    (C) STRANDEDNESS: single
948                    (D) TOPOLOGY: linear
949                (ii) MOLECULE TYPE: Primer DNA
950                (ix) FEATURE:
951                    (A ) NAME/KEY: AIPL1 primer
952                    (B) LOCATION:
953                    (D) OTHER INFORMATION:
954                (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:
955
956                    5'-gacacctccctttctcc-3'                    17
957
```

```
958            (2) INFORMATION FOR SEQ ID NO:45:
959                (i) SEQUENCE CHARACTERISTICS:
-->   960            (A) LENGTH: 18 bases
961                    (B) TYPE: nucleic acid
962                    (C) STRANDEDNESS: single
963                    (D) TOPOLOGY: linear
964                (ii) MOLECULE TYPE: Primer DNA (genomic) human
965                (ix) FEATURE:
966                    (A ) NAME/KEY: AIPL1 primer
967                    (B) LOCATION:
968                    (D) OTHER INFORMATION:
969                (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:
970
971                    5'-gctggggctgcctggctg-3'                    18
972
```

```
973            (2) INFORMATION FOR SEQ ID NO:46:
974                (i) SEQUENCE CHARACTERISTICS:
-->   975            (A) LENGTH: 20 bases
976                    (B) TYPE: nucleic acid
977                    (C) STRANDEDNESS: single
978                    (D) TOPOLOGY: linear
979                (ii) MOLECULE TYPE: Primer DNA (genomic) human
980                (ix) FEATURE:
981                    (A ) NAME/KEY: AIPL1 Primer
982                    (B) LOCATION:
983                    (D) OTHER INFORMATION:
984                (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:
985
986                    5'-ccgagtgattaccagaggga-3'                  20
987
```

```
988            (2) INFORMATION FOR SEQ ID NO:47:
989                (i) SEQUENCE CHARACTERISTICS:
-->   990            (A) LENGTH: 20 bases
991                    (B) TYPE: nucleic acid
```

992   (C) STRANDEDNESS: single
993   (D) TOPOLOGY: linear
994   (ii) MOLECULE TYPE: Primer DNA (genomic) human
995   (ix) FEATURE:
996   (A) NAME/KEY: AIPL1 Primer
997   (B) LOCATION:
998   (D) OTHER INFORMATION:
999   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:
1000
1001   5'-tgagctccagcacctcatag-3'   20
1002

1003   (2) INFORMATION FOR SEQ ID NO:48:
1004   (i) SEQUENCE CHARACTERISTICS:
--> 1005   (A) LENGTH: 18 bases
1006   (B) TYPE: nucleic acid
1007   (C) STRANDEDNESS: single
1008   (D) TOPOLOGY: linear
1009   (ii) MOLECULE TYPE: Primer DNA (genomic) human
1010   (ix) FEATURE:
1011   (A) NAME/KEY: AIPL1 primer
1012   (B) LOCATION:
1013   (D) OTHER INFORMATION:
1014   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:
1015
1016   5'-acgcagaggtgtggaatg-3'   18
1017

1018   (2) INFORMATION FOR SEQ ID NO:49:
1019   (i) SEQUENCE CHARACTERISTICS:
--> 1020   (A) LENGTH: 19 bases
1021   (B) TYPE: nucleic acid
1022   (C) STRANDEDNESS: single
1023   (D) TOPOLOGY: linear
1024   (ii) MOLECULE TYPE: Primer DNA (genomic) human
1025   (ix) FEATURE:
1026   (A) NAME/KEY: AIPL1 Primer
1027   (B) LOCATION:
1028   (D) OTHER INFORMATION:
1029   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:
1030
1031   5'-aaaaagtgacaccacgatc-3'   19
1032

1113   (2) INFORMATION FOR SEQ ID NO:55:
1114   (i) SEQUENCE CHARACTERISTICS:
--> 1115   (A) LENGTH: 6689 bases   35 (p. 7)
1116   (B) TYPE: nucleic acid
1117   (C) STRANDEDNESS: single
1118   (D) TOPOLOGY: linear
1119   (ii) MOLECULE TYPE: cDNA
1120   (ix) FEATURE:
1121   (A) NAME/KEY: AIPL1 gene exon/intron Acceptor

```
1122          splice site
1123              (B) LOCATION:
1124              (D) OTHER INFORMATION:
1125      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:
1126
1127              cactgacctgcagctctggggccagGTTGATGCCC          35
1128
```

```
1194      (2) INFORMATION FOR SEQ ID NO:60:
1195          (i) SEQUENCE CHARACTERISTICS:
1196              (A) LENGTH: 18 bases
1197              (B) TYPE: nucleic acid
1198              (C) STRANDEDNESS: single
1199              (D) TOPOLOGY: linear
1200         (ii) MOLECULE TYPE: DNA Primer
1201         (ix) FEATURE:
1202              (A ) NAME/KEY: AIPL1 gene Exon 1 Primer
1203              (B) LOCATION: 240
1204              (D) OTHER INFORMATION:
1205         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:
1206
1207              5'-ggacacctccctttctcc-3'                    18
1208
```

```
1209      (2) INFORMATION FOR SEQ ID NO:61:
1210          (i) SEQUENCE CHARACTERISTICS:
1211              (A) LENGTH: 18 bases
1212              (B) TYPE: nucleic acid
1213              (C) STRANDEDNESS: single
1214              (D) TOPOLOGY: linear
1215         (ii) MOLECULE TYPE: DNA Primer
1216         (ix) FEATURE:
1217              (A ) NAME/KEY: AIPL1 gene Exon 1 Primer
1218              (B) LOCATION: 240
1219              (D) OTHER INFORMATION:
1220         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:
1221
1222              5'-gctggggctgcctggctg-3'                    18
1223
```

```
1224      (2) INFORMATION FOR SEQ ID NO:62:
1225          (i) SEQUENCE CHARACTERISTICS:
1226              (A) LENGTH: 20 bases
1227              (B) TYPE: nucleic acid
1228              (C) STRANDEDNESS: single
1229              (D) TOPOLOGY: linear
1230         (ii) MOLECULE TYPE: DNA Primer
1231         (ix) FEATURE:
1232              (A ) NAME/KEY: AIPL1 gene Exon 2 Primer
1233              (B) LOCATION: 297
1234              (D) OTHER INFORMATION:
1235         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:
1236
```

INPUT SET: S36601.raw

1237   5'-gggccttgaacagtgtgtct-3'   20
1238

1239   (2) INFORMATION FOR SEQ ID NO:63:
1240   (i) SEQUENCE CHARACTERISTICS:
--> **1241**   **(A) LENGTH: 19 bases**
1242   (B) TYPE: nucleic acid
1243   (C) STRANDEDNESS: single
1244   (D) TOPOLOGY: linear
1245   (ii) MOLECULE TYPE: DNA Primer
1246   (ix) FEATURE:
1247   (A) NAME/KEY: AIPL1 gene Exon 2 Primer
1248   (B) LOCATION: 297
1249   (D) OTHER INFORMATION:
1250   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:
1251
1252   5'-tttcccgaaacacagcagc-3'   19
1253

1254   (2) INFORMATION FOR SEQ ID NO:64:
1255   (i) SEQUENCE CHARACTERISTICS:
--> **1256**   **(A) LENGTH: 18 bases**
1257   (B) TYPE: nucleic acid
1258   (C) STRANDEDNESS: single
1259   (D) TOPOLOGY: linear
1260   (ii) MOLECULE TYPE: DNA Primer
1261   (ix) FEATURE:
1262   (A) NAME/KEY: AIPL1 gene Exon 3 Primer
1263   (B) LOCATION: 364
1264   (D) OTHER INFORMATION:
1265   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:
1266
1267   5'-agtgagggagcaggattc-3'   18
1268

1269   (2) INFORMATION FOR SEQ ID NO:65:
1270   (i) SEQUENCE CHARACTERISTICS:
--> **1271**   **(A) LENGTH: 20 bases**
1272   (B) TYPE: nucleic acid
1273   (C) STRANDEDNESS: single
1274   (D) TOPOLOGY: linear
1275   (ii) MOLECULE TYPE: DNA Primer
1276   (ix) FEATURE:
1277   (A) NAME/KEY: AIPL1 gene Exon 3 Primer
1278   (B) LOCATION: 364
1279   (D) OTHER INFORMATION:
1280   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:
1281
1282   5'-tgcccatgatgcccgctgtc-3'   20
1283

1284   (2) INFORMATION FOR SEQ ID NO:66:
1285   (i) SEQUENCE CHARACTERISTICS:

next page

INPUT SET: S36601.raw

```
-->  1286           (A) LENGTH: 18 bases
     1287           (B) TYPE: nucleic acid
     1288           (C) STRANDEDNESS: single
     1289           (D) TOPOLOGY: linear
     1290       (ii) MOLECULE TYPE: DNA Primer
     1291       (ix) FEATURE:
     1292           (A ) NAME/KEY: AIPL1 gene Exon 4 Primer
     1293           (B) LOCATION: 315
     1294           (D) OTHER INFORMATION:
     1295       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
     1296
     1297           5'-tttcgggtctctgatggg-3'                          18
     1298
```

```
     1299    (2) INFORMATION FOR SEQ ID NO:67:
     1300        (i) SEQUENCE CHARACTERISTICS:
-->  1301           (A) LENGTH: 17 bases
     1302           (B) TYPE: nucleic acid
     1303           (C) STRANDEDNESS: single
     1304           (D) TOPOLOGY: linear
     1305       (ii) MOLECULE TYPE: DNA Primer
     1306       (ix) FEATURE:
     1307           (A ) NAME/KEY: AIPL1 gene Exon 4 Primer
     1308           (B) LOCATION: 315
     1309           (D) OTHER INFORMATION:
     1310       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:
     1311
     1312           5'-gcaggctcccagagtc-3'                            17
     1313
```

```
     1314    (2) INFORMATION FOR SEQ ID NO:68:
     1315        (i) SEQUENCE CHARACTERISTICS:
-->  1316           (A) LENGTH: 19 bases
     1317           (B) TYPE: nucleic acid
     1318           (C) STRANDEDNESS: single
     1319           (D) TOPOLOGY: linear
     1320       (ii) MOLECULE TYPE: DNA Primer
     1321       (ix) FEATURE:
     1322           (A ) NAME/KEY: AIPL1 gene Exon 5 Primer
     1323           (B) LOCATION: 279
     1324           (D) OTHER INFORMATION:
     1325       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:
     1326
     1327           5'-gcagctgcctcaggtcatg-3'                         19
     1328
```

```
     1329    (2) INFORMATION FOR SEQ ID NO:69:
     1330        (i) SEQUENCE CHARACTERISTICS:
-->  1331           (A) LENGTH: 18 bases
     1332           (B) TYPE: nucleic acid
     1333           (C) STRANDEDNESS: single
     1334           (D) TOPOLOGY: linear
     1335       (ii) MOLECULE TYPE: DNA Primer
```

```
1336          (ix) FEATURE:
1337               (A ) NAME/KEY: AIPL1 gene Exon 5 Primer
1338               (B) LOCATION: 279
1339               (D) OTHER INFORMATION:
1340          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:
1341
1342               5'-gtggggtggaaagaaaag-3'                        18
1343
```

```
1344     (2) INFORMATION FOR SEQ ID NO:70:
1345          (i) SEQUENCE CHARACTERISTICS:
-->  1346          (A) LENGTH: 18 bases
1347               (B) TYPE: nucleic acid
1348               (C) STRANDEDNESS: single
1349               (D) TOPOLOGY: linear
1350          (ii) MOLECULE TYPE: DNA Primer
1351          (ix) FEATURE:
1352               (A ) NAME/KEY: AIPL1 gene Exon 6 Primer
1353               (B) LOCATION: 497
1354               (D) OTHER INFORMATION:
1355          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:
1356
1357               5'-ctgggaagggagctgtag-3'                        18
1358
```

```
1359     (2) INFORMATION FOR SEQ ID NO:71:
1360          (i) SEQUENCE CHARACTERISTICS:
-->  1361          (A) LENGTH: 19 bases
1362               (B) TYPE: nucleic acid
1363               (C) STRANDEDNESS: single
1364               (D) TOPOLOGY: linear
1365          (ii) MOLECULE TYPE: DNA Primer
1366          (ix) FEATURE:
1367               (A ) NAME/KEY: AIPL1 gene Exon 6 Primer
1368               (B) LOCATION: 497
1369               (D) OTHER INFORMATION:
1370          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:
1371
1372               5'-aaaagtgacaccacgatcc-3'                       19
1373
```

```
1374     (2) INFORMATION FOR SEQ ID NO:72:
1375          (i) SEQUENCE CHARACTERISTICS:
1376               (A) LENGTH: 383 amino acids
1377               (B) TYPE: amino acid
1378               (D) TOPOLOGY: linear
1379          (ii) MOLECULE TYPE: protein
1380          (ix) FEATURE:
1381               (A ) NAME/KEY: Human Aipl1
1382               (B) LOCATION:
1383          (D) OTHER INFORMATION:
1384       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:
1385
```

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/765,061*

INPUT SET: S36601.raw

```
1386  Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr
1387    1               5                  10              15
1388  Ile Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly
1389                   20                 25              30
1390  Ser Arg Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu
1391                   35                 40              45
1392  Arg Thr Val Ile Asp Asp Ser Arg Gln Val Gly Gln Pro Met His
1393                   50                 55              60
1394  Ile Ile Ile Gly Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu
1395                   65                 70              75
1396  Leu Thr Ser Met Arg Val His Glu Val Ala Glu Phe Trp Cys Asp
1397                   80                 85              90
1398  Thr Ile His Thr Gly Val Tyr Pro Ile Leu Ser Arg Ser Leu Arg
1399                   95                 100             105
1400  Gln Met Ala Gln Gly Lys Asp Pro Thr Glu Trp His Val His Thr
1401                   110                115             120
1402  Cys Gly Leu Ala Asn Met Phe Ala Tyr His Thr Leu Gly Tyr Glu
1403                   125                130             135
1404  Asp Leu Asp Glu Leu Gln Lys Glu Pro Gln Pro Leu Val Phe Val
1405                   140                145             150
1406  Ile Glu Leu Leu Gln Val Asp Ala Pro Ser Asp Tyr Gln Arg Glu
1407                   155                160             165
1408  Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys Ala Val Pro Val
1409                   170                175             180
1410  Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly Arg Tyr Glu
1411                   185                190             195
1412  Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu Arg Asn
1413                   200                205             210
1414  Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys Leu
1415                   215                220             225
1416  Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu
1417                   230                235             240
1418  Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp
1419                   245                250             255
1420  Ile Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg
1421                   260                265             270
1422  Ala Arg Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala
1423                   275                280             285
1424  Asp Leu Gln Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala
1425                   290                295             300
1426  Val Arg Arg Glu Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys
1427                   305                310             315
1428  Gln Glu Glu Glu Arg Leu (Xxx)Cys Arg Asn Met Leu Ser Gln Gly
1429                   320                325             330
1430  Ala Thr Gln Pro Pro Ala Glu Pro Pro Thr Glu Pro Pro Ala Gln
1431                   335                340             345
1432  Ser Ser Thr Glu Pro Pro Ala Glu Pro Pro Thr Ala Pro Ser Ala
1433                   350                355             360
1434  Glu Leu Ser Ala Gly Pro Pro Ala Glu Pro Ala Thr Glu Pro Pro
1435                   365                370             375
1436  Pro Ser Pro Gly His Ser Leu Gln His
1437                   380              383
1438
```

```
1439        (2) INFORMATION FOR SEQ ID NO:73:
1440            (i) SEQUENCE CHARACTERISTICS:          } 384 ( next page)
--> 1441            (A) LENGTH: (369) amino acids
1442                (B) TYPE: amino acid
1443                (D) TOPOLOGY: linear
1444        (ii) MOLECULE TYPE: protein
1445        (ix) FEATURE:
1446                (A ) NAME/KEY: Chimpansee Aipl1
1447                (B) LOCATION:
1448                (D) OTHER INFORMATION:
1449        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:
1450

1451  Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr
1452    1           5               10              15
1453  Ile Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly
1454               20              25              30
1455  Ser Arg Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu
1456               35              40              45
1457  Arg Thr Val Ile Asp Asp Ser Arg Gln Val Gly Gln Pro Met His
1458               50              55              60
1459  Ile Ile Ile Gly Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu
1460               65              70              75
1461  Leu Thr Ser Met Arg Val His Glu Val Ala Glu Phe Trp Cys Asp
1462               80              85              90
1463  Thr Ile His Thr Gly Val Tyr Pro Ile Leu Ser Arg Ser Leu Arg
1464               95              100             105
1465  Gln Met Ala Gln Gly Lys Asp Pro Thr Glu Trp His Val His Thr
1466               110             115             120
1467  Cys Gly Leu Ala Asn Met Phe Ala Tyr His Thr Leu Gly Tyr Glu
1468               125             130             135
1469  Asp Leu Asp Glu Leu Gln Lys Glu Pro Gln Pro Leu Val Phe Val
1470               140             145             150
1471  Ile Glu Leu Leu Gln Val Asp Ala Pro Ser Asp Tyr Gln Arg Glu
1472               155             160             165
1473  Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys Ala Val Pro Val
1474               170             175             180
1475  Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly Arg Tyr Glu
1476               185             190             195
1477  Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu Arg Asn
1478               200             205             210
1479  Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys Leu
1480               215             220             225
1481  Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu
1482               230             235             240
1483  Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp
1484               245             250             255
1485  Ile Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg
1486               260             265             270
1487  Ala Arg Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala
1488               275             280             285
1489  Asp Leu Arg Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala
1490               290             295             300
```

INPUT SET: S36601.raw

```
1491   Val Arg Arg Glu Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys
1492                   305                 310                 315
1493   Gln Glu Glu Glu Arg Leu Arg Cys Arg Asn Met Leu Ser Gln Gly
1494                   320                 325                 330
1495   Ala Thr Gln Pro Pro Ala Glu Pro Pro Thr Glu Pro Pro Ala Gln
1496                   335                 340                 345
1497   Ser Ser Thr Glu Pro Pro Ala Glu Pro Pro Pro Ala Pro Ser Ala
1498                   350                 355                 360
1499   Glu Leu Ser Ala Gly Pro Pro Ala Glu Thr Ala Thr Glu Pro Pro
1500                   365                 370                 375
1501   Pro Ser Pro Gly His Ser Leu Gln His
1502                   365              369
1503                   380
```

```
1748        (2) INFORMATION FOR SEQ ID NO:78:
1749            (i) SEQUENCE CHARACTERISTICS:
1750                (A) LENGTH: 372 amino acids
1751                (B) TYPE: amino acid
1752                (D) TOPOLOGY: linear
1753            (ii) MOLECULE TYPE: protein
1754            (ix) FEATURE:
1755                (A ) NAME/KEY: Squirrel Monkey Aip11
1756                (B) LOCATION:
1757                (D) OTHER INFORMATION:
1758            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:
1759
1760   Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr
1761     1               5                10                15
1762   Ile Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly
1763                   20                25                30
1764   Ser Arg Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu
1765                   35                40                45
1766   Arg Thr Val Ile Asp Asp Ser Arg Glu Val Gly Gln Pro Met His
1767                   50                55                60
1768   Ile Ile Ile Gly Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu
1769                   65                70                75
1770   Leu Thr Ser Met Arg Val Arg Glu Val Ala Glu Phe Trp Cys Asp
1771                   80                85                90
1772   Thr Ile His Thr Gly Val Tyr Pro Ile Leu Ser Arg Ser Leu Arg
1773                   95                100               105
1774   Gln Met Ala Gln Gly Lys Asp Pro Thr Glu Trp His Val His Thr
1775                   110               115               120
1776   Cys Gly Leu Ala Asn Met Phe Ala Tyr His Thr Leu Gly Tyr Glu
1777                   125               130               135
1778   Asp Leu Asp Glu Leu Gln Lys Glu Pro Gln Pro Leu Ile Phe Val
1779                   140               145               150
1780   Ile Glu Leu Leu Gln Val Asp Ala Pro Ser Asp Tyr Gln Arg Glu
1781                   155               160               165
1782   Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys Val Val Pro Val
1783                   170               175               180
1784   Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly Arg Tyr Glu
1785                   185               190               195
1786   Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu Arg Asn
```

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/765,061*

INPUT SET: S36601.raw

```
1787                200              205              210
1788 Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys Leu
1789                215              220              225
1790 Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu
1791                230              235              240
1792 Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp
1793                245              250              255
1794 Ile Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg
1795                260              265              270
1796 Ala Arg Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala
1797                275              280              285
1798 Asp Leu Gln Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala
1799                290              295              300
1800 Val Arg Arg Glu Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys
1801                305              310              315
1802 Gln Glu Glu Glu Arg Leu Arg Cys Arg Asn Met Leu Ser Gln Gly
1803                320              325              330
1804 Ala Thr Trp Ser Pro Ala Glu Pro Ala Glu Pro Pro Ala Glu
1805                335              340              345
1806 Ser Ser Thr Glu Pro Pro Ala Glu Pro Ala Glu Pro Pro Ala
1807                350              355              360
1808 Glu Leu Thr Leu Thr Pro Gly His Pro Leu Gln His
1809                365              370
1810
```

number the amino acids under every 5 amino acids

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/765,061*

INPUT SET: S36601.raw

Line	Error	Original Text
4	Number of Sequences (1) Doesn't Equal Actual Count (78)	(iii) NUMBER OF SEQUENCES: 1
7	Entered (6749) and Calc. Seq. Length (6689) differ	(A) LENGTH: 6749 bases
130	# of Sequences for line conflicts w/ running total	ctggagctta gcctgagagg ggttcttgc
336	Entered (1129) and Calc. Seq. Length (1119) differ	(A) LENGTH: 1129 bases
366	# of Sequences for line conflicts w/ running total	gagctaacct tgaccccggg gcacccacta cagcactga
915	Entered (20) and Calc. Seq. Length (0) differ	(A) LENGTH: 20 bases
930	Entered (19) and Calc. Seq. Length (0) differ	(A) LENGTH: 19 bases
945	Entered (17) and Calc. Seq. Length (0) differ	(A) LENGTH: 17 bases
960	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18 bases
975	Entered (20) and Calc. Seq. Length (0) differ	(A) LENGTH: 20 bases
990	Entered (20) and Calc. Seq. Length (0) differ	(A) LENGTH: 20 bases
1005	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18 bases
1020	Entered (19) and Calc. Seq. Length (0) differ	(A) LENGTH: 19 bases
1115	Entered (6689) and Calc. Seq. Length (35) differ	(A) LENGTH: 6689 bases
1196	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18 bases
1211	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18 bases
1226	Entered (20) and Calc. Seq. Length (0) differ	(A) LENGTH: 20 bases
1241	Entered (19) and Calc. Seq. Length (0) differ	(A) LENGTH: 19 bases
1256	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18 bases
1271	Entered (20) and Calc. Seq. Length (0) differ	(A) LENGTH: 20 bases
1286	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18 bases
1301	Entered (17) and Calc. Seq. Length (0) differ	(A) LENGTH: 17 bases
1316	Entered (19) and Calc. Seq. Length (0) differ	(A) LENGTH: 19 bases
1331	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18 bases
1346	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18 bases
1361	Entered (19) and Calc. Seq. Length (0) differ	(A) LENGTH: 19 bases
1428	Wrong Amino Acid Designator	Gln Glu Glu Glu Arg Leu Xxx Cys Arg Asn Met Leu Ser G
1441	Entered (369) and Calc. Seq. Length (384) differ	(A) LENGTH: 369 amino acids

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION   *US/09/765,061*

INPUT SET: S36601.raw

APPLICANT
TITLE OF INVENTION
ADDRESSEE
STREET
CITY
STATE
COUNTRY
ZIP
CORRESPONDENCE ADDRESS
MEDIUM TYPE
COMPUTER
OPERATING SYSTEM
SOFTWARE
COMPUTER READABLE FORM
APPLICATION NUMBER
FILING DATE
CLASSIFICATION
CURRENT APPLICATION DATA
APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA